

AMENDMENTS TO THE CLAIMS

The following listing of claims will replace all prior versions, and listings, of claims in the application:

LISTING OF CLAIMS:

1. (Currently amended): A method of data analysis for determining a base sequence for nucleic acid, ~~electrophoresing~~ based on detected data of electrophoresis of a fragment sample of nucleic acid ~~and determining the base sequence of the nucleic acid on the basis of detected data,~~ comprising steps of:

(A) performing waveform shaping by Fourier transformation on data of a certain number N of points from the head of the detected data with a parameter of a previously set peak interval;

(B) determining the base sequence as to data of P points ($P < N$) from the head of the data of N points;

(C) obtaining a peak interval from the result of the sequence determination;

(D) performing waveform shaping by Fourier transformation on data of N points from a position returning by L points ($L < M$) from final data precedently subjected to the sequence determination with a parameter of a precedently obtained peak interval; and

(E) determining the base sequence as to data of M points ($M < N$) of a central portion among data of N points subjected to second or later waveform shaping, so as to be connected with data precedently subjected to the sequence determination ~~among data of N points subjected to second or later waveform shaping,~~ wherein

the steps (E) → (C) → (D) are repeated until data disappear or no analysis is required despite presence of data.

2. (Currently amended): The method of data analysis for determining a base sequence for nucleic acid according to claim 1, wherein

FFT treatment is applied to at least one of steps (A) or (D) as the waveform shaping by Fourier transformation.

3. (Currently amended): The method of data analysis for determining a base sequence for nucleic acid according to claim 2, assuming that N is equal to 2^n , M is equal to $2^{(n-1)}$ and L is equal to $2^{(n-2)}$.